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SEQUENCE LISTING

<110> Wolfrain, Lawrence A
Letterio, John J

<120> FUNCTIONALIZED TGF-BETA FUSION PROTEINS

<130> 4239-61302

<140> US 10/017,372

<141> 2001-10-19

<150> US 60/242,292

<151> 2000-10-20

<160> 39

<170> PatentIn version 3.2

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

ggagagatct ggtaccgaga tggcgccct

28

C1

<210> 2

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

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42

<210> 3

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

gactacaagg atgacgacga caaggccctg gataccaaact actgcttc

48

<210> 4

<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
cttgcgtcg tcatccttgt agtctcggcg gtgccggag ctgtg 45

<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
gactacaagg atgacgacga caggagaaga actgctgcgt gccgc 45

<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

C1
<220>
<223> Primer

<400> 6
cttgcgtcg tcatccttgt agtctcggcg gtgccggag ctgtg 45

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 7

Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 8
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

<220>
<221> CDS
<222> (1)..(1197)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (278)..(279)
<223> Maturation cleavage site (relates to amino acid residue nos.)

<400> 8
atg gcg cct tcg ggg ctg cg^g ctc ttg cc^g ctg ctg ctg cc^g ctg ctg 48
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu
1 5 10 15

tgg ctg cta gtg ctg ac^g cct gg^c cg^g cc^g gc^c gga ctg tcc acc 96
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

tgc aag acc atc gac atg gag ctg gtg aag cg^g aag cg^c atc gag gc^c 144
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

att cgc ggc cag att ctg tcc aag ctt cg^g ctt gc^c agc ccc cc^g agc 192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

cag ggg gac gtg cc^g ccc gg^c cg^g ctg cct gag gca gta ctg gct ctt 240
Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

C1 tac aac agt acc cgc gac cg^g gta gc^c ggg gaa agt gtc gaa cc^g gag 288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

ccc gag cca gag gc^c gac tac tac gc^c aag gag gtc acc cg^c gtg cta 336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

atg gtg gaa agc gg^c aac caa atc tat gat aaa ttc aag gg^c acc cc^c 384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

cac agc tta tat atg ctg ttc aac ac^g tcg gag ct^c cg^g gaa gc^c gtg 432
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

ccg gaa cct gta ttg ctc tct cg^g gca gag ctg cg^c ctg ctg agg ctc 480
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Arg Leu
145 150 155 160

aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat 528
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

gat tcc tgg cg^c tac ctc agc aac cg^g ctg ctg gc^c ccc agt gac tca 576
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser

180	185	190	
ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu 195 200 205			624
acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser 210 215 220			672
tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn 225 230 235 240			720
tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro 245 250 255			768
ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His 260 265 270			816
agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu 275 280 285			864
gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg 290 295 300			912
<i>C1</i> cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His 305 310 315 320			960
gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr 325 330 335			1008
atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn 340 345 350			1056
cag cac aac ccg ggc tcg gcg cgc ccg tgc tgc gtg ccc cag gcg Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala 355 360 365			1104
ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val 370 375 380			1152
gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser 385 390 395			1197

<210> 9
<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (*Sus scrofa*) TGF-beta1/N-terminal FLAG Fusion Construct

<400> 9

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu

195

200

205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu
275 280 285

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

<210> 10

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

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aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120
attcatgaac ccaaggggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
agcctagaca ctcagtagac caaggtccctg gctctgtaca accagcacaa cccgggcgcg 240
tcggcggcgc cgtgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg 300
ggccgcaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttcctg caagtgcagc 360
tga 363

<210> 11

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct

C1 <220>

<221> PEPTIDE

<222> (1)..(8)

<223> FLAG tag

<400> 11

Asp Tyr Lys Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
1 5 10 15

Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

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<210> 12
<211> 1197
<212> DNA
<213> Artificial Sequence
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<220>
<223> Porcine (*Sus scrofa*) TGF-beta1/FLAG (11/12) Fusion Construct

<220>
<221> CDS
<222> (1)..(1197)
<223> Protein coding sequence

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<220>
<221> misc_feature
<222> (278)..(279)
<223> Maturation cleavage site (relates to amino acid residue nos.)
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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu      48
1           5           10          15

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tgc aag acc atc gac atg gag ctg gtg aag cg_g aag cgc atc gag gcc 144
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

att cgc ggc cag att ctg tcc aag ctt cg^g ctt gcc agc ccc cc^g agc 192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

tac aac agt acc cgc gac cg_g gta gcc ggg gaa agt gtc gaa ccg gag 288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

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ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta      336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
          100           105           110

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atg gtc gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc
 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125 384

cac agc tta tat atg ctg ttc aac acg tcg gag ctc cg^g gaa gc^g gt^g
 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140 432

ccg gaa cct gta ttg ctc tct cg^g gca gag ctg cg^c ctg ctg agg ct^c
 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160 480

aag tta aaa gt^g gag cag cac gt^g gag cta tac cag aaa tac agc aat
 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175 528

gat tcc tgg cg^c tac ctc agc aac cg^g ctg ctg gcc ccc agt gac tca
 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190 576

ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gt^g cg^g cag tgg ct^g
 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205 624

acc cg^c aga gag gct ata gag ggt ttt cg^c ctc agt gcc cac tct tcc
 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 210 215 220 672

tct gac agc aaa gat aac aca ctc cac gt^g gaa att aac ggg ttc aat
 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240 720

tct ggc cg^c cg^g ggt gac ctg gcc acc att cac gg^c atg aac cg^g ccc
 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255 768

tt^c ctg ctc ctc atg gcc acc cc^g ctg gag agg gcc cag cac ctg cac
 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270 816

agc tcc cg^g cac cg^c cg^a gcc ctg gat acc aac tac tgc ttc agc tcc
 Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 275 280 285 864

acg gac tac aag gat gac gac aag gag aag aac tgc tgc gt^g cg^g
 Thr Asp Tyr Lys Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
 290 295 300 912

cag ctc tac att gac tt^c cg^g aag gac ctg ggc tgg aag tgg att cat
 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 305 310 315 320 960

gaa ccc aag ggc tac cat gcc aat tt^c tgc ctg ggg ccc tgt ccc tac
 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 325 330 335 1008

atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac
 1056

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

cag cac aac ccg ggc gcg tcg gcg ccg tgc tgc gtg ccg cag gcg 1104
Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg 1152
Leu Glu Pro Leu Pro Ile Val Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga 1197
Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

<210> 13

<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<400> 13

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

C1

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

C1 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
275 280 285

Thr Asp Tyr Lys Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
385 390 395

<210> 14
<211> 363
<212> DNA
<213> Artificial Sequence

<220>

<223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

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aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctgaaagtgg 120
attcatgaac ccaagggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
agcctagaca ctcagtacaa caaggtcctg gctctgtaca accagcacaa cccggcgcc 240
tcggcggcgc cgtgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg 300
ggccgcaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttcctg caagtgcagc 360
tga 363

C1
<210> 15
<211> 120
<212> PRT
<213> Artificial Sequence

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<223> Porcine (Sus scrofa) TGF-beta1/FLAG (11/12) Fusion Construct

<220>
<221> peptide
<222> (12)..(19)
<223> FLAG tag

<400> 15

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Asp Tyr Lys Asp Asp
1 5 10 15

Asp Asp Lys Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe

20

25

30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 16

<211> 1612

<212> DNA

<213> Artificial Sequence

C1 <220>

<223> Murine (*Mus musculus*) TGF-beta1/N+5 FLAG Fusion Construct

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<221> 5'UTR

<222> (1)..(347)

<223> 5' untranslated region

<220>

<221> CDS

<222> (348)..(1559)

<223> Protein coding sequence

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<221> misc_feature

<222> (1182)..(1196)

<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>

<221> misc_feature

<222> (1182)..(1159)

<223> Encodes mature fusion protein

<220>

<221> misc_feature
 <222> (1197)..(1220)
 <223> Encodes FLAG epitope tag

<220>
 <221> 3'UTR
 <222> (1560)..(1612)
 <223> 3' untranslated region

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ctccctcgga	cctgctggca	gtagctccc	tatttaagaa	cacccactt	tggatctcag	120
agagcgctca	tctcgatttt	taccctggtg	gtatactgag	acaccttggt	gtcagagcct	180
caccgcgact	cctgctgctt	tctccctcaa	cctcaaatta	ttcaggacta	tcacctacct	240
ttccttggga	gaccacccc	cacaagccct	gcaggggcgg	ggcctccgca	tcccacctt	300
gccgagggtt	cccgctctcc	gaagtgccgt	ggggcgccgc	ctccccc	atg ccg ccc	356
					Met Pro Pro	
					1	
tcg ggg ctg	ctg cgg cta	ctg ccg ctt	ctg ctc cca	ctc ccg tgg	ctt cta	404
Ser Gly Leu	Arg Leu Leu	Pro Leu Leu	Leu Pro	Leu Pro	Trp Leu Leu	
5	10	15				
gtg ctg acg ccc	ggg agg cca	gcc gcg gga	ctc tcc acc	tgc aag acc		452
Val Leu Thr	Pro Gly Arg	Pro Ala Ala	Gly Leu Ser	Thr Cys Lys	Thr	
20	25	30	35			
atc gac atg gag	ctg gtg aaa	cgg aag cgc	atc gaa gcc	atc cgt ggc		500
Ile Asp Met Glu	Leu Val Lys	Arg Lys Arg	Ile Glu Ala	Ile Arg Gly		
40	45	50				
cag atc ctg tcc	aaa cta agg	ctc agt ccc	cca agc cag	ggg gag		548
Gln Ile Leu Ser	Lys Leu Arg	Leu Ala Ser	Pro Pro Ser	Gln Gly Glu		
55	60	65				
gta ccg ccc	ggc ccg ctg	ccc gag gcg	gtg ctc gct	ttg tac aac	agc	596
Val Pro Pro	Gly Pro Leu	Pro Glu Ala	Val Leu Ala	Leu Tyr Asn	Ser	
70	75	80				
acc cgc gac	cgg gtg gca	ggc gag agc	gcc gac cca	gag ccg	gag ccc	644
Thr Arg Asp	Arg Val Ala	Gly Glu Ser	Ala Asp Pro	Glu Pro	Glu Pro	
85	90	95				
gaa gcg gac	tac tat gct	aaa gag gtc	acc cgc	gtg cta	atg gtg gac	692
Glu Ala Asp	Tyr Tyr Ala	Lys Glu Val	Thr Arg Val	Leu Met Val	Asp	
100	105	110	115			
cgc aac aac	gcc atc tat	gag aaa acc	aaa gac	atc tca	cac agt ata	740
Arg Asn Asn	Ala Ile Tyr	Glu Lys Thr	Lys Asp Ile	Ser His	Ser Ile	
120	125	130				
tat atg ttc	ttc aat acg	tca gac att	cg gaa gca	gtg ccc	gaa ccc	788

C1

Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro
 135 140 145

cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt 836
 Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser
 150 155 160

gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg 884
 Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
 165 170 175

cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg 932
 Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp
 180 185 190 195

ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga 980
 Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly
 200 205 210

gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc 1028
 Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser
 215 220 225

aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt 1076
 Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg
 230 235 240

cg^{Cl} gg^{Cl} gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc 1124
 Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu
 245 250 255

ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg 1172
 Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg
 260 265 270 275

cac cgg aga gcc ctg gat acc aac gac tac aag gat gac gac gac aag 1220
 His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp Asp Lys
 280 285 290

gcc ctg gat acc aac tat tgc ttc agc tcc aca gag aag aac tgc tgt 1268
 Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
 295 300 305

gtg cgg cag ctg tac att gac ttt agg aag gac ctg ggt tgg aag tgg 1316
 Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
 310 315 320

atc cac gag ccc aag ggc tac cat gcc aac ttc tgt ctg gga ccc tgc 1364
 Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
 325 330 335

ccc tat att tgg agc ctg gac aca cag tac agc aag gtc ctt gcc ctc 1412
 Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
 340 345 350 355

tac aac caa cac aac ccg ggc gct tcg gcg tca ccg tgc tgc gtg ccg 1460
 Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro

360

365

370

cag gct ttg gag cca ctg ccc atc gtc tac tac gtg ggt cgc aag ccc 1508
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
375 380 385

aag gtg gag cag ttg tcc aac atg att gtg cgc tcc tgc aag tgc agc 1556
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
390 395 400

tga agccccgccc cgccccgccc ctcccgccag gccccggcccc gcccccgccc cgc 1612

<210> 17

<211> 403

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine (Mus musculus) TGF-beta1/N+5 FLAG Fusion Construct

<400> 17

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

C1

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

<210> 18
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gccctggata ccaacgacta caaggatgac gacgacaagg ccctggatac caactactgc 60
ttcagctcca cg 73

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

C1

<220>
<223> Primer

<400> 19
cttgcgtcg tcatccattgt agtcgttatac cagggctcg 60
caggtgctgg gc 72

<210> 20
<211> 1624
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta1/N+5 HA Fusion Construct

<220>
<221> 5'UTR
<222> (1)..(347)
<223> 5' untranslated region

<220>
<221> CDS

<222> (348)..(1571)
 <223> Protein coding sequence

 <220>
 <221> misc_feature
 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

 <220>
 <221> misc_feature
 <222> (1182)..(1571)
 <223> Encodes mature fusion protein

 <220>
 <221> misc_feature
 <222> (1197)..(1232)
 <223> Encodes HA epitope tag

 <220>
 <221> 3'UTR
 <222> (1572)..(1624)
 <223> 3' untranslated region

 <400> 20
 ccccaagcctg cctcttgagt ccctcgcatc ccaggaccct ctctccccg agagggcagat 60
 ctccctcgga cctgctggca gtagctcccc tatttaagaa cacccacttt tggatctcag 120
 agagcgctca tctcgatttt taccctggtg gtatactgag acacccctt gtcagagcct 180
 caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240
 ttccttggga gaccccaccc cacaaggccct gcaggggcgg ggcctccgca tcccacctt 300
 gccgagggtt cccgctctcc gaagtgcgtt gggcgccgc ctccccc atg cc Met Pro Pro 356
 1

 tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404
 Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Pro Trp Leu Leu
 5 10 15

 gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc 452
 Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr
 20 25 30 35

 atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc 500
 Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
 40 45 50

 cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag 548
 Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
 55 60 65

 gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc 596
 Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
 70 75 80

acc cgc gac cggt gca ggc gag agc gcc gac cca gag ccg gag ccc	644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro	
85 90 95	
gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac	692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp	
100 105 110 115	
cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata	740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile	
120 125 130	
tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc	788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro	
135 140 145	
cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt	836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser	
150 155 160	
gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg	884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp	
165 170 175	
cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg	932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp	
180 185 190 195	
ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga	980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly	
200 205 210	
C gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc	1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser	
215 220 225	
aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt	1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg	
230 235 240	
cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc	1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu	
245 250 255	
ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg	1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg	
260 265 270 275	
cac cgg aga gcc ctg gat acc aac agc tac cca tac gac gtg cca gac	1220
His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp Val Pro Asp	
280 285 290	
tac gca tct ctg gcc ctg gat acc aac tat tgc ttc agc tcc aca gag	1268
Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu	
295 300 305	

aag aac tgc tgt gtg cgg cag ctg tac att gac ttt agg aag gac ctg Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu	310 315 320	1316
ggt tgg aag tgg atc cac gag ccc aag ggc tac cat gcc aac ttc tgt Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys	325 330 335	1364
ctg gga ccc tgc ccc tat att tgg agc ctg gac aca cag tac agc aag Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys	340 345 350 355	1412
gtc ctt gcc ctc tac aac caa cac aac ccg ggc gct tcg gcg tca ccg Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro	360 365 370	1460
tgc tgc gtg ccg cag gct ttg gag cca ctg ccc atc tac tac tac gtg Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val	375 380 385	1508
ggt cgc aag ccc aag gtg gag cag ttg tcc aac atg att gtg cgc tcc Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser	390 395 400	1556
tgc aag tgc agc tga agccccgcccc cgccccgcccc ctcccccgcag gccccggcccc Cys Lys Cys Ser	405	1611
ccccccgcccc cgc		1624

<210> 21
 <211> 407
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Murine (Mus musculus) TGF-beta1/N+5 HA Fusion Construct

 <400> 21

 Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser

290

295

300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

C) Val Arg Ser Cys Lys Cys Ser
405

<210> 22

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

gccctggata ccaacagcta cccatacgac gtgccagact acgcatctct ggccctggat 60

accaactact gcttcagctc cacggagaag aactgctgct tgccggcag 108

<210> 23

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

cagagatgcg tagtctggca cgtcgtatgg gtagctgttg gtatccaggg ctccggcggtg 60

ccgggagctg tgc 73

<210> 24
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta2/N+5 FLAG Fusion Construct

<220>
<221> CDS
<222> (1)..(1284)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (907)..(921)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
<221> misc_feature
<222> (907)..(1284)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (922)..(945)
<223> Encodes FLAG epitope tag

C1
<400> 24
atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg gtc ccg 48
Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1 5 10 15

gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat cag ttt 96
Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc aag ctg 144
Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag gtc ccc 192
Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
50 55 60

ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg cag gag 240
Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

aag gca agc cgg agg gca gcc tgc gag cgc gag cgg agc gag cag 288
Lys Ala Ser Arg Arg Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc cac ctc 336

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
 100 105 110

ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac ttc aga 384
 Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
 115 120 125

atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg aat ctg 432
 Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
 130 135 140

gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa gcc aga 480
 Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
 145 150 155 160

gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc aaa gac 528
 Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
 165 170 175

tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg aaa acc 576
 Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
 180 185 190

aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct gtg cag 624
 Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
 195 200 205

C1
 gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata agt tta 672
 Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
 210 215 220

cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc atc ccg 720
 His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
 225 230 235 240

aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat ggc acc 768
 Asn Lys Ser Glu Glu Leu Ala Arg Phe Ala Gly Ile Asp Gly Thr
 245 250 255

tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act agg aaa 816
 Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
 260 265 270

aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg ccc tcc 864
 Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
 275 280 285

tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc gct ttg 912
 Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
 290 295 300

gat gct gcc gac tac aag gat gac gac gac aag gct ttg gat gct gcc 960
 Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala
 305 310 315 320

tac tgc ttt aga aat gtg cag gat aat tgc tgc ctt cgc cct ctt tac 1008
 Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr

325	330	335	
att gat ttt aag agg gat ctt gga tgg aaa tgg atc cat gaa ccc aaa Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys 340	345	350	1056
ggg tac aat gct aac ttc tgt gct ggg gca tgc cca tat cta tgg agt Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser 355	360	365	1104
tca gac actcaa cac acc aaa gtc ctc agc ctg tac aac acc ata aat Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn 370	375	380	1152
ccc gaa gct tcc gct tcc cct tgc tgt gtg tcc cag gat ctg gaa cca Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro 385	390	395	400
ctg acc att ctc tat tac att gga aat acg ccc aag atc gaa cag ctt Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu 405	410	415	1248
tcc aat atg att gtc aag tct tgt aaa tgc agc taa Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser 420	425		1284

C1
<210> 25

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine (Mus musculus) TGF-beta2/N+5 FLAG Fusion Construct

<400> 25

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro		
1	5	10
		15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe		
20	25	30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu		
35	40	45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro		
50	55	60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu		
65	70	75
		80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

C1 Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Asp Tyr Lys Asp Asp Asp Lys Ala Leu Asp Ala Ala

305

310

315

320

Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
340 345 350

Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
355 360 365

Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
405 410 415

Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425

C1

<210> 26

<211> 1303

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine (*Mus musculus*) TGF-beta2/N+5 HA Fusion Construct

<220>

<221> 5'UTR

<222> (1)..(7)

<223> 5' untranslated region

<220>

<221> CDS

<222> (8)..(1303)

<223> Protein coding sequence

<220>

<221> misc_feature

<222> (914)..(928)

<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>

<221> misc_feature

<222> (914)..(1303)
 <223> Encodes mature fusion protein

 <220>
 <221> misc_feature
 <222> (929)..(964)
 <223> Encodes HA epitope tag

 <400> 26
 taaaaaac atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg 49
 Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu
 1 5 10

 gtc ccg gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat 97
 Val Pro Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp
 15 20 25 30

 cag ttt atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc 145
 Gln Phe Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser
 35 40 45

 aag ctg aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag 193
 Lys Leu Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu
 50 55 60

 gtc ccc ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg 241
 Val Pro Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu
 65 70 75

 C1
 cag gag aag gca agc cgg agg gca gcc gcc tgc gag cgc gag ccg agc 289
 Gln Glu Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser
 80 85 90

 gag cag gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc 337
 Glu Gln Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser
 95 100 105 110

 cac ctc ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac 385
 His Leu Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr
 115 120 125

 ttc aga atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg 433
 Phe Arg Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser
 130 135 140

 aat ctg gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa 481
 Asn Leu Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys
 145 150 155

 gcc aga gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc 529
 Ala Arg Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser
 160 165 170

 aaa gac tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg 577
 Lys Asp Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val
 175 180 185 190

aaa acc aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct 625
 Lys Thr Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala
 195 200 205

 gtg cag gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata 673
 Val Gln Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile
 210 215 220

 agt tta cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc 721
 Ser Leu His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile
 225 230 235

 atc ccg aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat 769
 Ile Pro Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp
 240 245 250

 ggc acc tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act 817
 Gly Thr Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr
 255 260 270

 agg aaa aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg 865
 Arg Lys Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu
 275 280 285

 ccc tcc tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc 913
 Pro Ser Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg
 290 295 300

C1
 gct ttg gat gct gcc agc tac cca tac gac gtg cca gac tac gca tct 961
 Ala Leu Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 305 310 315

 ctg gct ttg gat gct gcc tac tgc ttt aga aat gtg cag gat aat tgc 1009
 Leu Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys
 320 325 330

 tgc ctt cgc cct ctt tac att gat ttt aag agg gat ctt gga tgg aaa 1057
 Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys
 335 340 345 350

 tgg atc cat gaa ccc aaa ggg tac aat gct aac ttc tgt gct ggg gca 1105
 Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala
 355 360 365

 tgc cca tat cta tgg agt tca gac act caa cac acc aaa gtc ctc agc 1153
 Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser
 370 375 380

 ctg tac aac acc ata aat ccc gaa gct tcc gct tcc cct tgc tgt gtg 1201
 Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val
 385 390 395

 tcc cag gat ctg gaa cca ctg acc att ctc tat tac att gga aat acg 1249
 Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr
 400 405 410

 ccc aag atc gaa cag ctt tcc aat atg att gtc aag tct tgt aaa tgc 1297

Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys
415 420 425 430

agc taa 1303
Ser

<210> 27
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta2/N+5 HA Fusion Construct

<400> 27

Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

C1 Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala
305 310 315 320

Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu
325 330 335

Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile
340 345 350

His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro
355 360 365

Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr
370 375 380

Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln
385 390 395 400

Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys
405 410 415

Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425 430

<210> 28
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 FLAG Fusion Construct

<220>
<221> CDS
<222> (1)..(1272)
<223> Protein coding sequence

C1
<220>
<221> misc_feature
<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (895)..(1272)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (910)..(933)
<223> Encodes FLAG epitope tag

<400> 28
atg cac ttg caa agg gct ctg gta gtc ctg gcc ctg ctg aac ttg gcc 48
Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192
Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

tat cag gtc ctg gca ctt tac aac agc acc cg^g gag ttg ctg gaa gag 240
 Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct 288
 Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg 336
 Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag 384
 Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg 432
 Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag 480
 Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag 528
 Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
 165 170 175

C1
 cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg 576
 His Ile Ala Lys Gln Arg Tyr Ile Gly Lys Asn Leu Pro Thr Arg
 180 185 190

ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag 624
 Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
 195 200 205

tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac 672
 Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
 210 215 220

tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt 720
 Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
 225 230 235 240

cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac 768
 His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
 245 250 255

cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac 816
 His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
 260 265 270

aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc 864
 Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
 275 280 285

cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat gac Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp	912
290 295 300	
tac aag gat gac gac aag gcc ctg gac acc aat tac tgc ttc cgc Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg	960
305 310 315 320	
aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat att gac ttc cgg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg	1008
325 330 335	
cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag ggt tac tat gcc Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala	1056
340 345 350	
aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc gca gac aca acc Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr	1104
355 360 365	
cat agc acg gtg ctt gga cta tac aac acc ctg aac cca gag gcg tct His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser	1152
370 375 380	
gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc ctg acc atc ttg Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu	1200
385 390 395 400	
C1 tac tat gtg ggc aga acc ccc aag gtg gag cag ctg tcc aac atg gtg Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val	1248
405 410 415	
gtg aag tcg tgt aag tgc agc tga Val Lys Ser Cys Lys Cys Ser	1272
420	

<210> 29
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 FLAG Fusion Construct
<400> 29

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
290 295 300

Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
305 310 315 320

Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
325 330 335

Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
340 345 350

Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
355 360 365

His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser
370 375 380

C1
Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
385 390 395 400

Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val
405 410 415

Val Lys Ser Cys Lys Cys Ser
420

<210> 30
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 HA Fusion Construct

<220>
<221> CDS
<222> (1)..(1284)
<223> Protein coding sequence

<220>
<221> misc_feature

<222> (895)..(909)
<223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
<221> misc_feature
<222> (895)..(1284)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (910)..(945)
<223> Encodes HA epitope tag

<400> 30 48
atg cac ttg caa agg gct ctg gta gtc ctg gcc ctg aac ttg gcc
Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192
Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

C1 tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag 240
Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct 288
Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg 336
Glu Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag 384
Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg 432
Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag 480
Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag 528
Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg 576
 His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
 180 185 190

 ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag 624
 Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
 195 200 205

 tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac 672
 Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
 210 215 220

 tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt 720
 Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
 225 230 235 240

 cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac 768
 His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
 245 250 255

 cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac 816
 His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
 260 265 270

 aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc 864
 Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
 275 280 285

C1
 cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat agc 912
 Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
 290 295 300

 tac cca tac gac gtg cca gac tac gca tct ctg gcc ctg gac acc aat 960
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
 305 310 315 320

 tac tgc ttc cgc aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat 1008
 Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
 325 330 335

 att gac ttc cgg cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag 1056
 Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
 340 345 350

 ggt tac tat gcc aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc 1104
 Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
 355 360 365

 gca gac aca acc cat agc acg gtg ctt gga cta tac aac acc ctg aac 1152
 Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
 370 375 380

 cca gag gcg tct gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc 1200
 Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
 385 390 395 400

ctg acc atc ttg tac tat gtg ggc aga acc ccc aag gtg gag cag ctg 1248
Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
405 410 415

tcc aac atg gtg gtg aag tcg tgt aag tgc agc tga 1284
Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
420 425

<210> 31
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine (Mus musculus) TGF-beta3/N+5 HA Fusion Construct

<400> 31

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala
1 5 10 15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

C | Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
290 295 300

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
305 310 315 320

Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
325 330 335

Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
340 345 350

Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
355 360 365

Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
385 390 395 400

Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
405 410 415

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
420 425

<210> 32
<211> 1349
<212> DNA
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<220>
<221> 5'UTR
<222> (1)..(10)
<223> 5' untranslated region

<220>
<221> CDS
<222> (11)..(1222)
<223> Protein coding sequence

C1
<220>
<221> misc_feature
<222> (845)..(859)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (845)..(1222)
<223> Encodes mature fusion protein

<220>
<221> misc_feature
<222> (860)..(883)
<223> Encodes FLAG epitope tag

<220>
<221> 3'UTR
<222> (1223)..(1349)
<223> 3' untranslated region

<400> 32
tggtaccgag atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
1 5 10

49

ccg ctg ctg tgg ctg cta gtg acg cct ggc cg_g ccg gcc g_c gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cg_g aag cg_c 145
 Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
 30 35 40 45

atc gag gcc att cg_c ggc cag att ctg tcc aag ctt cg_g ctt gcc agc 193
 Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

ctg gct ctt tac aac agt acc cg_c gac cg_g gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

gaa ccg gag ccc gag cca gag g_c gac tac tac gcc aag gag gtc acc 337
 Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
 95 100 105

cg_c gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag 385
 Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
 110 115 120 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cg_g 433
 Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
 130 135 140

C1
 gaa g_c g_c gtg ccg gaa cct gta ttg ctc tct cg_g gca gag ctg cg_c ctg 481
 Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu
 145 150 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa 529
 Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
 160 165 170

tac agc aat gat tcc tgg cg_c tac ctc agc aac cg_g ctg ctg gcc ccc 577
 Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
 175 180 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cg_g 625
 Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
 190 195 200 205

cag tgg ctg acc cg_c aga gag gct ata gag ggt ttt cg_c ctc agt gcc 673
 Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
 210 215 220

cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac 721
 His Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
 225 230 235

ggg ttc aat tct ggc cg_c cg_g ggt gac ctg gcc acc att cac ggc atg 769

Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
 240 245 250

aac cgg ccc ttc ctg ctc atg gcc acc ccg ctg gag agg gcc cag 817
 Asn Arg Pro Phe Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
 255 260 265

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac tac 865
 His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr
 270 275 280 285

aag gat gac gac aag gcc ctg gat acc aac tac tgc ttc agc tcc 913
 Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 290 295 300

acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg aag 961
 Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
 305 310 315

gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc aat 1009
 Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
 320 325 330

ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag tac 1057
 Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
 335 340 345

agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg gcg 1105
 Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
 350 355 360 365

C1 gcg ccg tgc tgc gtg ccg cag cgc ctg gag cca ctg ccc atc gtg tac 1153
 Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
 370 375 380

tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc gtg 1201
 Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
 385 390 395

cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc cccgcccacc 1252
 Arg Ser Cys Lys Cys Ser
 400

cggcaggccc ggccccaccc cccggccct caccggggct gtatttaagg acatcgtgcc 1312

ccaagcccac ttgggatcga ttaaagcggc cgcgact 1349

<210> 33
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<400> 33

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

C1 Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

<210> 34
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct

<220>
 <221> 5'utr
 <222> (1)..(14)
 <223> 5' untranslated region

<220>
 <221> CDS
 <222> (15)..(1226)
 <223> Protein coding sequence

<220>
 <221> misc_feature
 <222> (849)..(863)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
 <221> misc_feature
 <222> (849)..(1226)
 <223> Encodes mature fusion protein

<220>
 <221> misc_feature
 <222> (864)..(887)
 <223> Encodes FLAG epitope tag

<220>
 <221> 3'UTR
 <222> (1227)..(1353)
 <223> 3' untranslated region

<400> 34 gatctggta c g a g at g g c g c c t tc g g g g ct g c g c t c tt g c c g ct g ct g Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu 1 5 10	50
ct g c g c t g ct g c t a g t g ct g a c g c c t g g c g c g g c c Leu Pro Leu Leu Trp Leu Leu Val Thr Pro Gly Arg Pro Ala Ala 15 20 25	98
g g a c t g t c c a c c t g a a g a c c a t c g a c t g g a g c g g a a g Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys 30 35 40	146
c g c a t c g a g g c c t t c g t c c a a g c t t c g c t t g c c Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala 45 50 55 60	194
a g c c c c g a g c a g g g g a c g t g c c g c c g c t g c c t g a g g c a Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala 65 70 75	242
g t a c t g g c t t a c a a c a g t a c c c g g a c c g g t a g c c g g g g a a g t Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser 80 85 90	290
g t c g a a c c g g a g c c c g a g g c g g a c t a c t a c g c c a a g g a g g c t Val Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val	338

95	100	105	
acc cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe			386
110	115	120	
aag ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu			434
125	130	135	140
cgg gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc Arg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg			482
145	150	155	
ctg ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag Leu Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln			530
160	165	170	
aaa tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc Lys Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala			578
175	180	185	
ccc agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val			626
190	195	200	
cgg cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt Arg Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser			674
205	210	215	220
gcc cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att Ala His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile			722
225	230	235	
aac ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc Asn Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly			770
240	245	250	
atg aac cgg ccc ttc ctg ctc atg gcc acc ccg ctg gag agg gcc Met Asn Arg Pro Phe Leu Leu Met Ala Thr Pro Leu Glu Arg Ala			818
255	260	265	
cag cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac Gln His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp			866
270	275	280	
tac aag gat gac gac aag gcc ctg gat acc aac tac tgc ttc agc Tyr Lys Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser			914
285	290	295	300
tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg			962
305	310	315	
aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala			1010
320	325	330	

aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln	1058
335 340 345	
tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser	1106
350 355 360	
gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val	1154
365 370 375 380	
tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile	1202
385 390 395	
gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc cccgccccacc Val Arg Ser Cys Lys Cys Ser	1256
400	
cggcaggccc ggccccaccc ccgccccct caccggggct gtatttaagg acatcgtgcc	1316
ccaagcccac ttgggatcga ttaaagcggc cgcgact	1353

<210> 35
<211> 403
<212> PRT
<213> Artificial Sequence

C1
<220>
<223> Porcine (Sus scrofa) TGF-beta1/N+5 FLAG Fusion Construct
<400> 35

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Pro Leu Leu	
1 5 10 15	

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr	
20 25 30	

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala	
35 40 45	

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser	
50 55 60	

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu	
65 70 75 80	

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu	
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85

90

95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

C1
Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

<210> 36
<211> 1361
<212> DNA
<213> Artificial Sequence

C1

<220>
<223> Porcine (*Sus scrofa*) TGF-beta1/N+5 HA Fusion Construct

<220>
<221> 5'UTR
<222> (1)..(10)
<223> 5' untranslated region

<220>
<221> CDS
<222> (11)..(1234)
<223> Protein coding sequence

<220>
<221> misc_feature
<222> (845)..(859)
<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
<221> misc_feature
<222> (845)..(1234)
<223> Encodes mature fusion protein

<220>
<221> misc_feature

<222> (860)..(895)
<223> Encodes HA epitope tag

<220>

<221> 3'UTR

<222> (1235)..(1361)

<223> 3' untranslated region

<400> 36

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu 49
1 5 10

ccg ctg ctg tgg ctg cta gtg acg cct ggc cggttgc gcc gca
Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly 97
15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cggttgc aag cggttgc
Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg 145
30 35 40 45

atc gag gcc att cgccggc cag att ctg tcc aag ctt cggttgc ctt gcc agc
Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser 193
50 55 60

ccc ccg agc cag ggg gac gtg ccgttgc ccc ggc ccgttgc cct gag gca gta
Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val 241
65 70 75

ctg gct ctt tac aac agt acc cgccggc gac ccgttgc gta gcc ggg gaa agt gtc
Leu Ala Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val 289
80 85 90

gaa ccg gag ccc gag cca gag gac tac tac gcc aag gag gtc acc
Glu Pro Glu Pro Glu Pro Ala Asp Tyr Ala Lys Glu Val Thr 337
95 100 105

cgccgttgc cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttccaa
Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys 385
110 115 120 125

ggc acc ccc cac agc tta tat atg ctg ttccaa acg tcg gag ctc ccgttgc
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg 433
130 135 140

gaa gcg gtg ccgttgc gaa cct gta ttgc ccgttgc ctt ccgttgc gca gag ctg
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu 481
145 150 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys 529
160 165 170

tac agc aat gat tcc tgg cgccgttgc tac ctc agc aac ccgttgc ccgttgc
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro 577
175 180 185

C1

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg 625
 Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
 190 195 200 205

 cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc 673
 Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
 210 215 220

 cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac 721
 His Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
 225 230 235

 ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg 769
 Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
 240 245 250

 aac cgg ccc ttc ctg ctc atg gcc acc cgg ctg gag agg gcc cag 817
 Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
 255 260 265

 cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac 865
 His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr
 270 275 280 285

 cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac 913
 Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr
 290 295 300

C1
 tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att 961
 Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile
 305 310 315

 gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc 1009
 Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly
 320 325 330

 tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta 1057
 Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu
 335 340 345

 gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg 1105
 Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro
 350 355 360 365

 ggc gcg tcg gcg cgc tgc tgc gtg ccc cag gcg ctg gag cca ctg 1153
 Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
 370 375 380

 ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc 1201
 Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
 385 390 395

 aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc 1254
 Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 400 405

 cccgcccacc cggcaggccc ggccccaccc cggcccgccct caccggggct gtatttaagg 1314

acatcgtgcc ccaagccac ttgggatcga ttaaagcggc cgcgact

1361

<210> 37
<211> 407
<212> PRT
<213> Artificial Sequence

<220>
<223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct

<400> 37

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

C1 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

ctg gct ctt tac aac agt acc cgc gac cggt gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc 337
 Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
 95 100 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag 385
 Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
 110 115 120 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg 433
 Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg
 130 135 140

gaa gcg gtg ccg gaa cct qta ttg ctc tct cgg gca gag ctg cgc ctg 481
 Glu Ala Val Pro Glu Pro Val Leu Ser Arg Ala Glu Leu Arg Leu
 145 150 155

ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa 529
 Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys
 160 165 170

C1 tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc 577
 Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro
 175 180 185

agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg 625
 Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg
 190 195 200 205

cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc 673
 Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala
 210 215 220

cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att aac 721
 His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn
 225 230 235

ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg 769
 Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met
 240 245 250

aac cgg ccc ttc ctg ctc atg gcc acc cgg ctg gag agg gcc cag 817
 Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
 255 260 265

cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac 865
 His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr

270	275	280	285	
cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr 290		295	300	913
tgc ttc agc tcc acg gag aag aac tgc tgc gtg cggtt cag ctc tac att Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile 305	310		315	961
gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly 320	325	330		1009
tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu 335	340	345		1057
gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro 350	355	360	365	1105
ggc gcg tcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu 370	375		380	1153
ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc Pro Ile Val Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser 385	390		395	1201
aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccggcc cgcccacagc Asn Met Ile Val Arg Ser Cys Lys Cys Ser 400	405			1254
cccgccccacc cggcaggccc ggccccaccc cccggccct caccggggct gtatttaagg				1314
acatcgtgcc ccaagccac ttgggatcga tttaagcggc cgcgact				1361
<210> 39				
<211> 407				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> Porcine (Sus scrofa) TGF-beta1/N+5 HA Fusion Construct				
<400> 39				
Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu 1	5	10	15	
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr 20	25		30	

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His

260

265

270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405